

Sequence listings:

SEQUENCE LISTING

Applicant: Garvan Institute of Medical Research

Title of Invention: A potential effector for the Grb7 family of signalling proteins.

Current Application Number:

Current Filing Date:

Prior Application Number: P09388

Prior Application Filing Date: 1997-09-23

Number of ID SEQ Nos: 2

Software: PatentIn Ver. 2.0

SEQ ID NO: 1

Length: 3400

Type: DNA

Organism: Homo sapiens

Sequence: 1

| | | | | | | |
|-------------|------------|-------------|------------|-------------|-------------|------|
| attcctcttc | ataatgcatg | ctcttttgg | catgctgaag | tagtcaatct | ccttttgcga | 60 |
| catggtgcag | accccaatgc | tgcagataat | tggaattata | ctcctctcca | tgaagctgca | 120 |
| attaaaggaa | agattgatgt | ttgcatgtgt | ctgttacagc | atggagctga | gccaaccatc | 180 |
| cgaaatacag | atggaaggac | agcattggat | ttagcagatc | catctgccaa | agcagtgcct | 240 |
| actggtgaat | ataagaaaga | tgaactctta | gaaagtgcc | ggagtggcaa | tgaagaaaaa | 300 |
| atgatggctc | tactcacacc | attaatgtc | aactgccacg | caagtgatgg | cagaaagtca | 360 |
| actccattac | atttggcagc | aggatataac | agagtaaaga | ttgtacagct | gttactgcaa | 420 |
| catggacgtg | atgtccatgc | taaagataaa | ggtgatctgg | taccattaca | caatgcctgt | 480 |
| tcttatggtc | attatgaagt | aactgaactt | ttggtcaagc | atggtggtgt | tgtaaatgca | 540 |
| atggacttgt | ggcaattcac | tcctcttcat | gaggcagctt | ctaagaacag | ggttgaagta | 600 |
| tgttctcttc | tcttaagtta | tggtgcagac | ccaacactgc | tcaattgtaa | gaataaaaag | 660 |
| gctatagact | tggtctccac | accacagtta | aaagaaagat | tagcatatga | atttaaaggc | 720 |
| cactcgttgc | tgcaagctgc | acgagaagct | gatgttactc | gaatcaaaaa | acatctctct | 780 |
| ctggaatgg | tgaatttcaa | gcctcctcaa | acacatgaaa | cagcattgca | ttgtgctgct | 840 |
| gcattctccat | atcccaaaag | aaagcaaata | tgtgaactgt | tgctaagaaa | aggagcaaac | 900 |
| atcaatgaaa | agactaaaga | attcttgact | cctctgcacg | tggtcatctga | gaaagctcat | 960 |
| aatgatgttg | ttgaagtgt | ggtgaaacat | gaagcaaagg | ttaatgctct | ggataatctt | 1020 |
| ggtcagactt | ctctacacag | agctgcatat | tgtggtcatc | tacaaaacctg | ccgcctactc | 1080 |
| ctgagctatg | ggtgtgatcc | taacattata | tccttccagg | gctttactgc | tttacagatg | 1140 |
| ggaaatgaaa | atgtacagca | actcctccaa | gagggatatc | cattaggtaa | ttcagaggca | 1200 |
| gacagacaat | tgctggaagc | tgcaaaggct | ggagatgtcg | aaactgtaaa | aaaactgtgt | 1260 |
| actgttcaga | gtgtcaactg | cagagacatt | gaaggcgctc | agtctacacc | acttcatttt | 1320 |
| gcagctgggt | ataacagagt | gtccgtggtg | gaatatctgc | tacagcatgg | agctgatgtg | 1380 |
| catgctaaag | ataaaggagg | ccttgtacct | ttgcacaatg | catgttctta | cggacattat | 1440 |
| gaagttgcag | aacttcttgt | taaacatgga | gcagtagtta | atgtagctga | tttatggaaa | 1500 |
| tttacacctt | tacatgaagc | agcagcaaaa | ggaaaatatg | aaatttgcaa | acttctgctc | 1560 |
| cagcatgggtg | cagaccctac | aaaaaaaaac | agggatggaa | atactccttt | ggatcttggt | 1620 |
| aaagatggag | atacagatat | tcaagatcag | cttaggggag | atgcagcttt | gctagatgct | 1680 |
| gccaagaagg | gttgttttag | cagagtgaag | aagtgtctct | ctcctgataa | tgtaaaattgc | 1740 |
| cgcgataccc | aaggcagaca | ttcaaacacct | ttacatttag | cagctgggta | taataattta | 1800 |
| gaagttgcag | agtatttgtt | acaacacgga | gctgatgtga | atgcccaaga | caaaggagga | 1860 |
| cttatctctt | tacataatgc | agcatcttac | gggcatgtag | atgtagcagc | tctactaata | 1920 |

aagtataatg catctctcaa tgcacaggac aaatggggtt tcacaccttt gcacgaagca 1980
gccccaaaagg gacgaacaca gctttgtgct ttgttgctag cccatggagc tgacccgact 2040
cttaaaaatc aggaaggaca aacaccttta gatttagttt cagcagatga tgtcagcgct 2100
cttctgacag cagccatgcc cccatctgct ctgccccttt gttacaagcc tcaagtgttc 2160
aatgggtgtga gaagcccagg agccactgca gatgctctct cttcaggtrc atctagacca 2220
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ggagtagatt ttagcataac tcaattcgta aggaatcttg gacttgagca cctaattggat 2400
atatttgaga gagaacagat cactttggat gtattagtgg agatggggca caaggagctg 2460
aaggagattg gaatcaatgc ttatggacat aggcacaaac taattaaagg agtcgagaga 2520
cttatctccg gacaacaagg tcttaaccca tatttaactt tgaacacctc tggtagtggga 2580
acaattctta tagatctgtc tcctgatgat aaagagtttc agtctgtgga ggaagagatg 2640
caaagtlacag ttcgagagca cagagatgga ggtcatgcag gtggaatctt caacagatac 2700
aatattctca agattcagaa gggttgtaac aagaaactat gggaaagata cactcaccgg 2760
agaaaagaag tttctgaaga aaaccacaac catgccaatg aacgaatgct attcataggg 2820
tctccttttg tgaatgcaat tatccacaaa ggctttgatg aaaggcatgc gtacataggt 2880
ggtatgtttg gagctggcat ttattttgct gaaaactctt ccaaaagcaa tcaatatgta 2940
tatggaattg gaggaggtac tgggtgtcca gttcacaaag acagatcttg ttacatttgc 3000
cacaggcagc tgctcttttg cccggtaacc ttgggaaagt ctttctctga gttcagtgc 3060
atgaaaatgg cacattctcc tccagggtcat cactcagtcg ctggtagggc cagtgtaaa 3120
ggcctagcat tagctgaata tgttatttac agaggagaa aggcttatcc tgagtattta 3180
attacttacc agattatgag gctgaaggt atggtcagtg gataaatagt tattttaaga 3240
aactaattcc actgaacctt aaatcatcaa agcagagtg gcctctacgt tttactcctt 3300
tgctgaaaaa aaatcatctt gcccacaggc ctgtgcgcaa aggataaaaa tgtgaacgaa 3360
gtttaacatt ctgacttgat aaagctttaa taatgtacag 3400

SEQ ID NO: 2
Length: 1074
Type: PRT
Organism: Homo sapiens

Sequence: 2

Ile Pro Leu His Asn Ala Cys Ser Phe Gly His Ala Glu Val Val Asn
1 5 10 15
Leu Leu Leu Arg His Gly Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn
20 25 30
Tyr Thr Pro Leu His Glu Ala Ala Ile Lys Gly Lys Ile Asp Val Cys
35 40 45
Ile Val Leu Leu Gln His Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp
50 55 60
Gly Arg Thr Ala Leu Asp Leu Ala Asp Pro Ser Ala Lys Ala Val Leu
65 70 75 80
Thr Gly Glu Tyr Lys Lys Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly
85 90 95
Asn Glu Glu Lys Met Met Ala Leu Leu Thr Pro Leu Asn Val Asn Cys
100 105 110
His Ala Ser Asp Gly Arg Lys Ser Thr Pro Leu His Leu Ala Ala Gly
115 120 125
Tyr Asn Arg Val Lys Ile Val Gln Leu Leu Leu Gln His Gly Arg Asp
130 135 140
Val His Ala Lys Asp Lys Gly Asp Leu Val Pro Leu His Asn Ala Cys

15

145 150 155 160
Ser Tyr Gly His Tyr Glu Val Thr Glu Leu Leu Val Lys His Gly Gly
165 170 175
Cys Val Asn Ala Met Asp Leu Trp Gln Phe Thr Pro Leu His Glu Ala
180 185 190
Ala Ser Lys Asn Arg Val Glu Val Cys Ser Leu Leu Leu Ser Tyr Gly
195 200 205
Ala Asp Pro Thr Leu Leu Asn Cys Lys Asn Lys Ser Ala Ile Asp Leu
210 215 220
Ala Pro Thr Pro Gln Leu Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly
225 230 235 240
His Ser Leu Leu Gln Ala Ala Arg Glu Ala Asp Val Thr Arg Ile Lys
245 250 255
Lys His Leu Ser Leu Glu Met Val Asn Phe Lys His Pro Gln Thr His
260 265 270
Glu Thr Ala Leu His Cys Ala Ala Ser Pro Tyr Pro Lys Arg Lys
275 280 285
Gln Ile Cys Glu Leu Leu Leu Arg Lys Gly Ala Asn Ile Asn Glu Lys
290 295 300
Thr Lys Glu Phe Leu Thr Pro Leu His Val Ala Ser Glu Lys Ala His
305 310 315 320
Asn Asp Val Val Glu Val Val Val Lys His Glu Ala Lys Val Asn Ala
325 330 335
Leu Asp Asn Leu Gly Gln Thr Ser Leu His Arg Ala Ala Tyr Cys Gly
340 345 350
His Leu Gln Thr Cys Arg Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn
355 360 365
Ile Ile Ser Leu Gln Gly Phe Thr Ala Leu Gln Met Gly Asn Glu Asn
370 375 380
Val Gln Gln Leu Leu Gln Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala
385 390 395 400
Asp Arg Gln Leu Leu Glu Ala Ala Lys Ala Gly Asp Val Glu Thr Val
405 410 415
Lys Lys Leu Cys Thr Val Gln Ser Val Asn Cys Arg Asp Ile Glu Gly
420 425 430
Arg Gln Ser Thr Pro Leu His Phe Ala Ala Gly Tyr Asn Arg Val Ser
435 440 445
Val Val Glu Tyr Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp
450 455 460
Lys Gly Gly Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr

16

465 470 475 480
Glu Val Ala Glu Leu Leu Val Lys His Gly Ala Val Val Asn Val Ala
485 490 495
Asp Leu Trp Lys Phe Thr Pro Leu His Glu Ala Ala Ala Lys Gly Lys
500 505 510
Tyr Glu Ile Cys Lys Leu Leu Leu Gln His Gly Ala Asp Pro Thr Lys
515 520 525
Lys Asn Arg Asp Gly Asn Thr Pro Leu Asp Leu Val Lys Asp Gly Asp
530 535 540
Thr Asp Ile Gln Asp Leu Leu Arg Gly Asp Ala Ala Leu Leu Asp Ala
545 550 555 560
Ala Lys Lys Gly Cys Leu Ala Arg Val Lys Lys Leu Ser Ser Pro Asp
565 570 575
Asn Val Asn Cys Arg Asp Thr Gln Gly Arg His Ser Thr Pro Leu His
580 585 590
Leu Ala Ala Gly Tyr Asn Asn Leu Glu Val Ala Glu Tyr Leu Leu Gln
595 600 605
His Gly Ala Asp Val Asn Ala Gln Asp Lys Gly Gly Leu Ile Pro Leu
610 615 620
His Asn Ala Ala Ser Tyr Gly His Val Asp Val Ala Ala Leu Leu Ile
625 630 635 640
Lys Tyr Asn Ala Ser Leu Asn Ala Thr Asp Lys Trp Ala Phe Thr Pro
645 650 655
Leu His Glu Ala Ala Gln Lys Gly Arg Thr Gln Leu Cys Ala Leu Leu
660 665 670
Leu Ala His Gly Ala Asp Pro Thr Leu Lys Asn Gln Glu Gly Gln Thr
675 680 685
Pro Leu Asp Leu Val Ser Ala Asp Asp Val Ser Ala Leu Leu Thr Ala
690 695 700
Ala Met Pro Pro Ser Ala Leu Pro Ser Cys Tyr Lys Pro Gln Val Leu
705 710 715 720
Asn Gly Val Arg Ser Pro Gly Ala Thr Ala Asp Ala Leu Ser Ser Gly
725 730 735
Pro Ser Ser Pro Ser Ser Leu Ser Ala Ala Ser Ser Leu Asp Asn Leu
740 745 750
Ser Gly Ser Phe Ser Glu Leu Ser Ser Val Val Ser Ser Ser Gly Thr
755 760 765
Glu Gly Ala Ser Ser Leu Glu Lys Lys Glu Val Pro Gly Val Asp Phe
770 775 780
Ser Ile Thr Gln Phe Val Arg Asn Leu Gly Leu Glu His Leu Met Asp

17

785 790 795 800
Ile Phe Glu Arg Glu Gln Ile Thr Leu Asp Val Leu Val Glu Met Gly
805 810 815
His Lys Glu Leu Lys Glu Ile Gly Ile Asn Ala Tyr Gly His Arg His
820 825 830
Lys Leu Ile Lys Gly Val Glu Arg Leu Ile Ser Gly Gln Gln Gly Leu
835 840 845
Asn Pro Tyr Leu Thr Leu Asn Thr Ser Gly Ser Gly Thr Ile Leu Ile
850 855 860
Asp Leu Ser Pro Asp Asp Lys Glu Phe Gln Ser Val Glu Glu Glu Met
865 870 875 880
Gln Ser Thr Val Arg Glu His Arg Asp Gly Gly His Ala Gly Gly Ile
885 890 895
Phe Asn Arg Tyr Asn Ile Leu Lys Ile Gln Lys Val Cys Asn Lys Lys
900 905 910
Leu Trp Glu Arg Tyr Thr His Arg Arg Lys Glu Val Ser Glu Glu Asn
915 920 925
His Asn His Ala Asn Glu Arg Met Leu Phe His Gly Ser Pro Phe Val
930 935 940
Asn Ala Ile Ile His Lys Gly Phe Asp Glu Arg His Ala Tyr Ile Gly
945 950 955 960
Gly Met Phe Gly Ala Gly Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser
965 970 975
Asn Gln Tyr Val Tyr Gly Ile Gly Gly Gly Thr Gly Cys Pro Val His
980 985 990
Lys Asp Arg Ser Cys Tyr Ile Cys His Arg Gln Leu Leu Phe Cys Arg
995 1000 1005
Val Thr Leu Gly Lys Ser Phe Leu Gln Phe Ser Ala Met Lys Met Ala
1010 1015 1020
His Ser Pro Pro Gly His His Ser Val Thr Gly Arg Pro Ser Val Asn
1025 1030 1035 1040
Gly Leu Ala Leu Ala Glu Tyr Val Ile Tyr Arg Gly Glu Gln Ala Tyr
1045 1050 1055
Pro Glu Tyr Leu Ile Thr Tyr Gln Ile Met Arg Pro Glu Gly Met Val
1060 1065 1070
Asp Gly